CLAIMS

We claim:

1. A method of typing a group B streptococcal bacterium, wherein the method comprises analysing the nucleotide sequence of one or more regions of a gene selected from the group consisting of *cpsD, cpsE, cpsF. cpsG* and *cpsI/M* genes of said bacterium, said region(s) comprising one or more nucleotides whose sequence varies between types of group B streptococcal bacteria.

2. The method according to claim 1, wherein the nucleotide sequence is analysed at one or more of positions 62, 78-86, 138, 139, 144, 198, 204, 211, 281, 240, 249, 300, 321, 419, 429, 437, 457, 466, 486, 602, 606; 627, 636, 645, 803, 971, 1026, 1044, 1173, 1194, 1251, 1278, 1413, 1495, 1500, 1501, 1512, 1518, 1527, 1595, 1611, 1620, 1627, 1629, 1655, 1832, 1856, 1866, 1871, 1892, 1971, 2026, 2088, 2134, 2187 or 2196 as shown in Figure 1.

3. The method according to claim 1, wherein at least one region is within a sequence delineated by the 3' 136 bases of the *cpsE* gene and the 5' 218 bases of *cpsG* of a *cpsE-cpsF-cspG* gene cluster of said streptococcal bacterium.

4. The method according to claim 3, wherein the nucleotide sequence is analysed at one or more of positions 1413, 1495, 1500, 1501, 1512, 1518, 1527, 1595, 1611, 1620, 1627, 1629, 1655, 1832, 1856, 1866, 1871, 1892, 1971, 2026, 2088, 2134, 2187 or 2196 as shown in Figure 1.

5. The method according to claim 1, wherein at least one region is within the *cpsI/M* genes of said bacterium.

6. The method according to claim 1, wherein analyzing the nucleotide sequence comprises sequencing said one or more regions.

7. The method according to claim 1, wherein analyzing the nucleotide sequence comprises determining whether a polynucleotide obtained from said bacterium selectively hybridises to a polynucleotide probe comprising one or more of the said regions.

8. The method according to claim 1, wherein analyzing the nucleotide sequence comprises determining whether the polynucleotide obtained from said bacterium selectively hybridises to one or more of a plurality of polynucleotide probes corresponding to one or more of the said regions.

9. The method according to claim 8, wherein the plurality of polynucleotide probes is present as a microarray.

10. The method according to claim 1, wherein analyzing the nucleotide sequence comprises an amplification step using one or more primers, at least one of which hybridises specifically to a sequence which differs between types of group B streptococcal bacteria.

11. The method according to claim 1, wherein analyzing the nucleotide sequence comprises an amplification step using primer pairs, at least one of which hybridises specifically to a sequence which differs between types of group B streptococcal bacteria.

12. The method according to claim 10, wherein said primers are selected from the primers shown in Table 2.

13. The method according to claim 11, wherein said primers are selected from the primers shown in Table 2.

14. A method of typing a group B streptococcal bacterium, wherein the method comprises determining the presence or absence, in the genome of said bacterium, of one or more surface protein genes selected from the group consisting of *rib, alp2* and *alp3* genes.

15. The method according to claim 14, wherein determining the presence or absence of said surface protein genes comprises determining whether a polynucleotide obtained from said bacterium selectively hybridises to a polynucleotide probe corresponding to a region of said surface protein genes.

16. The method according to claim 14, wherein determining the presence or absence of said surface protein genes comprises an amplification step using one or more primers which amplify a region of said surface protein genes.

17. The method according to claim 16 wherein said primers are selected from the primers shown in Table 6.

18. The method according to claim 1, which further comprises determining the presence or absence, in the genome of said bacterium, of one or more surface protein genes selected from the group consisting of *rib, alp2* and *alp3* genes.

19. A method of typing a group B streptococcal bacterium, wherein the method comprises determining the presence or absence, in the genome of said bacterium, of one or more mobile genetic elements selected from the group consisting of IS*861*, IS*1548*, IS*1381*, ISSa*4* and GBSi1.

20. The method according to claim 19, wherein determining the presence or absence of said mobile genetic elements comprises determining whether a polynucleotide obtained from said bacterium selectively hybridises to a polynucleotide probe corresponding to a region of said mobile genetic elements.

21. The method according to claim 19, wherein determining the presence or absence of said mobile genetic elements comprises an amplification step using one or more primers which amplify a region of said mobile genetic elements.

22. The method according to claim 21, wherein said primers are selected from the primers shown in Table 10.

23. The method according to claim 14, which further comprises determining the presence or absence, in the genome of said bacterium, of one or more mobile genetic elements selected from the group consisting of IS*861*, IS*1548*, IS*1381*, ISSa*4* and GBSi1.

24. A polynucleotide consisting essentially of at least 10 contiguous nucleotides of a region within a *cpsD-cpsE-cpsF-cpsG* gene cluster of a group B streptococcal bacterium, said polynucleotide comprising one or more nucleotides which differ(s) between group B streptococcal serotypes.

25. The polynucleotide according to claim 24, wherein said nucleotides which differ between group B streptococcal serotypes are at one or more of positions 62, 78-86, 138, 139, 144, 198, 204, 211, 281, 240, 249, 300, 321, 419, 429, 437, 457, 466, 486, 602, 606, 627, 636, 645, 803, 971, 1026, 1044, 1173, 1194, 1251, 1278, 1413, 1495, 1500, 1501, 1512, 1518, 1527, 1595, 1611, 1620, 1627, 1629, 1655, 1832, 1856, 1866, 1871, 1892, 1971, 2026, 2088, 2134, 2187 and 2196 as shown in Figure 1.

26. A polynucleotide consisting essentially of at least 10 contiguous nucleotides of a region within a sequence delineated by the 3' 136 base pairs of *cpsE* and the 5' 218 base pairs of *cpsG* of a *cpsE-cpsF-cspG* gene cluster of a group B streptococcal bacterium, said polynucleotide comprising one or more nucleotides which differ(s) between group B streptococcal types.

27. The polynucleotide according to claim 26, wherein said nucleotides which differ between group B streptococcal types correspond to one or more of positions 1413, 1495, 1500, 1501, 1512, 1518, 1527, 1595, 1611, 1620, 1627, 1629, 1655, 1832, 1856, 1866, 1871, 1892, 1971, 2026, 2088, 2134, 2187 and 2196 as shown in Figure 1.

28. A polynucleotide consisting essentially of at least 10 contiguous nucleotides corresponding to a region within a *cpsI/M* gene of a group B streptococcal bacterium, said polynucleotide comprising one or more nucleotides which differ(s) between streptococcal serotypes.

29. The polynucleotide according to claim 28, wherein the polynucleotide is selected from the nucleotide sequences shown in Table 2.

30. A polynucleotide consisting essentially of at least 10 contiguous nucleotides of a region within a *rib, alp2* or *alp3* gene of a group B streptococcal bacterium, said polynucleotide comprising one or more nucleotides which differ(s) between group B streptococcal subtypes.

31. The polynucleotide according to claim 30, wherein the polynucleotide is selected from the nucleotide sequences shown in Table 6.

32. A composition comprising a plurality of polynucleotides according to any one of claims 24 to 31.

33. A microarray comprising a plurality of polynucleotides according to any one of claims 24 to 31.